Hands On : Using MaBoSS with WebMaBoSS

Vincent Noël[1]

[1]Computational Systems Biology of Cancer,
Institut Curie, INSERM U900, Mines ParisTech, PSL Research University, Paris

Computational Systems Biology for Complex Human Disease
from static to dynamic representations of disease mechanisms

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institut Curie

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La science pour la santé
From science to health

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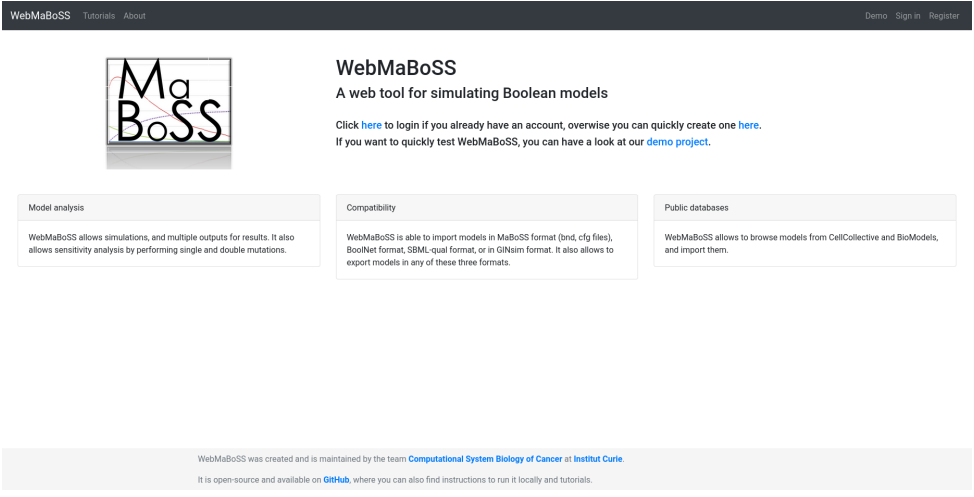
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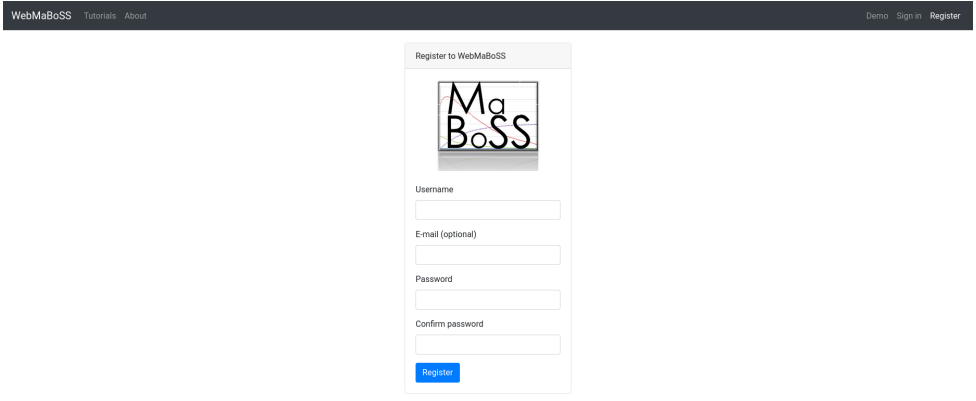
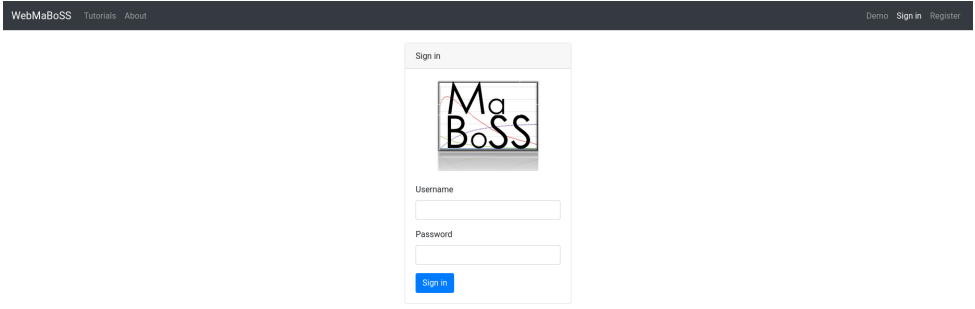
WebMaBoSS
A web tool for simulating Boolean models
Click here to login if you already have an account, overwise you can quickly create one here.
If you want to quickly test WebMaBoSS, you can have a look at our demo project.
Model analysis
WebMaBoSS allows simulations, and multiple outputs for results. It also allows sensitivity analysis by performing single and double mutations.
Compatibility
WebMaBoSS is able to import models in MaBoSS format (bnd, cfg files), BoolNet format, SBML-qual format, or in GINsim format. It also allows to export models in any of these three formats.
Public databases
WebMaBoSS allows to browse models from CellCollective and BioModels, and import them.
WebMaBoSS was created and is maintained by the team Computational System Biology of Cancer at Institut Curie.
It is open-source and available on GitHub, where you can also find instructions to run it locally and tutorials.

Create an account



Logging in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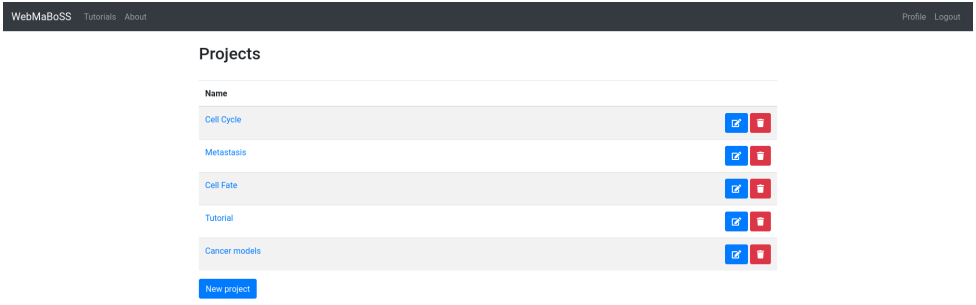
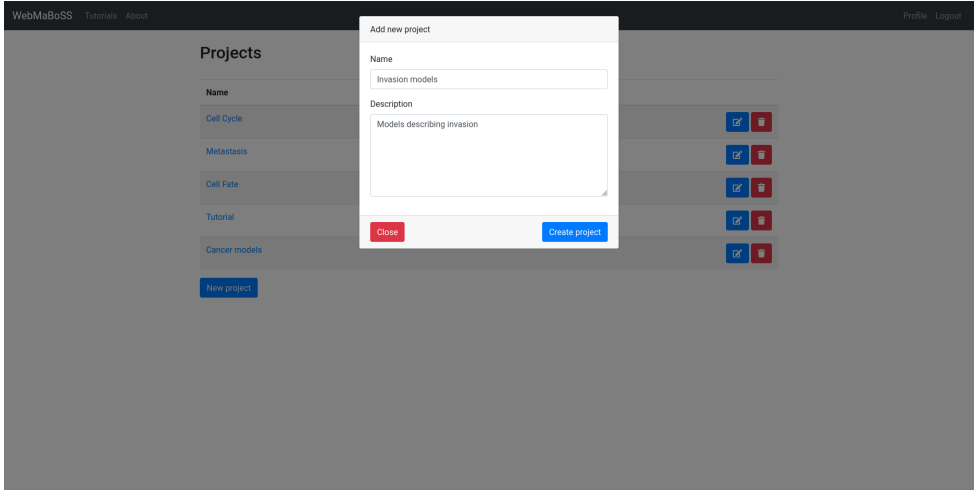
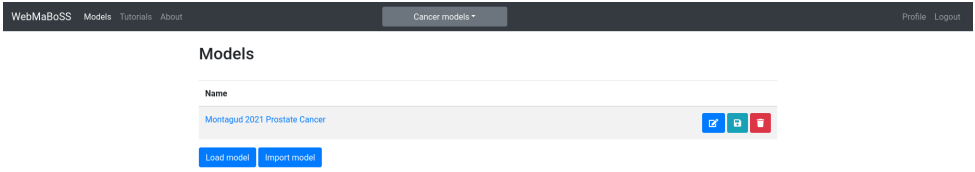
List of projects



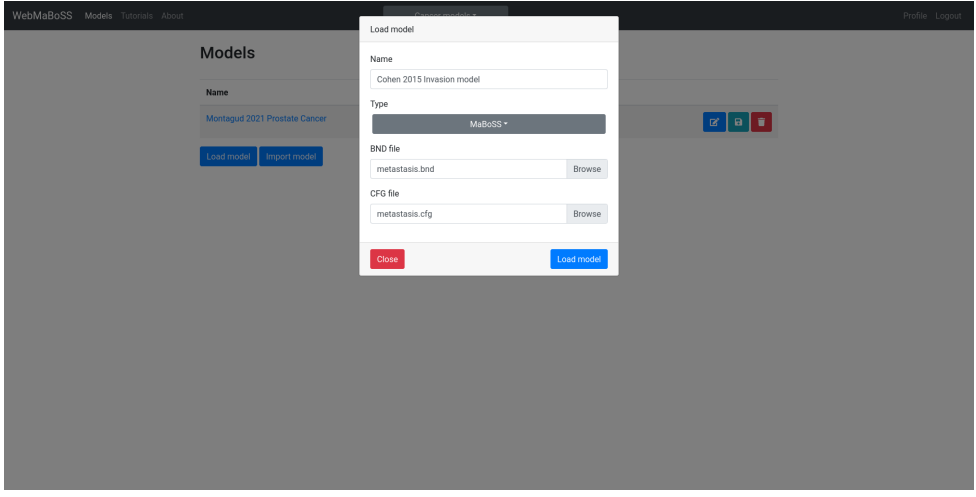
Creating a project



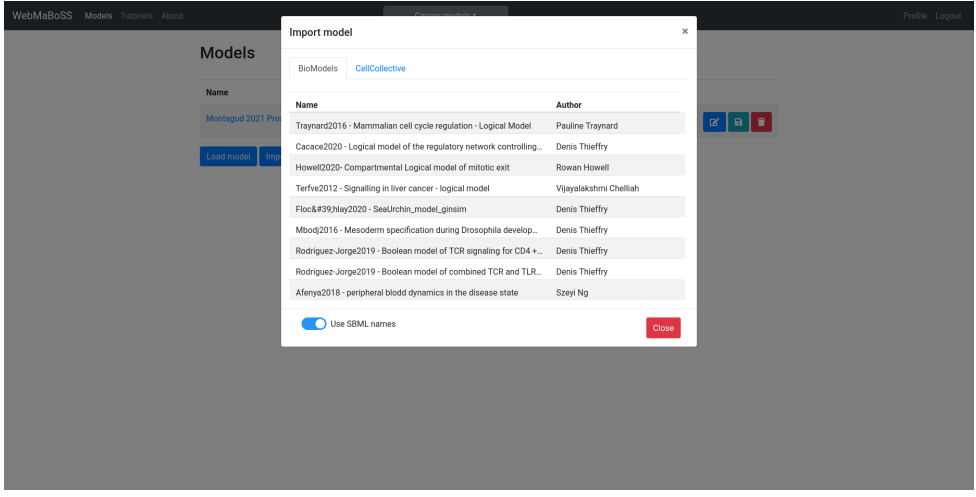
- List of models



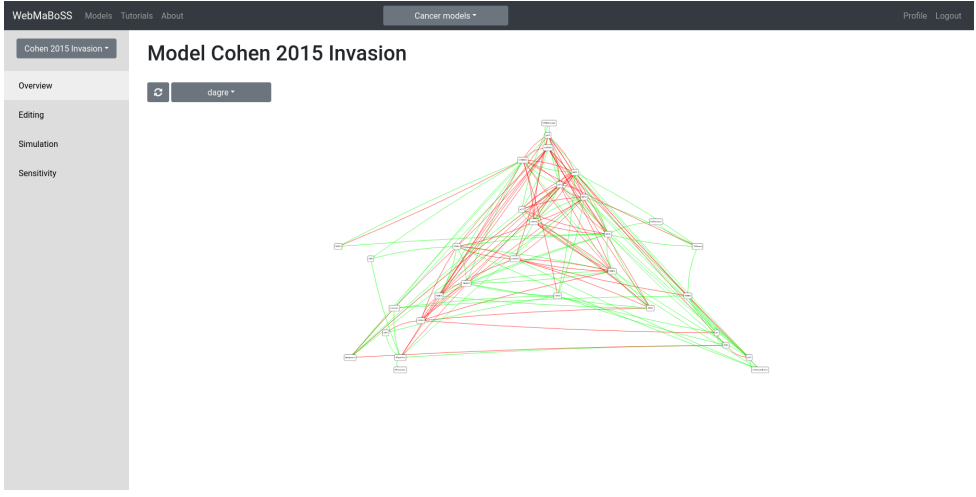
Loading a model



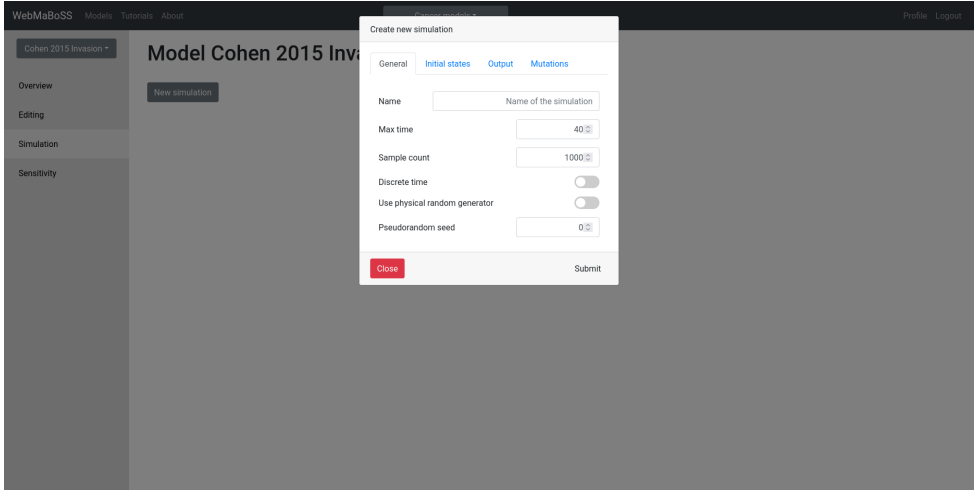
Importing a model



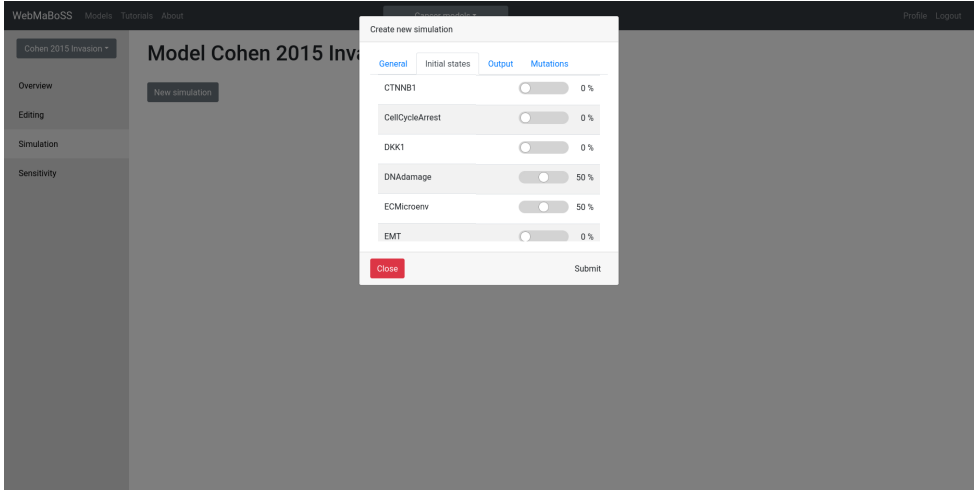
Model interaction graph



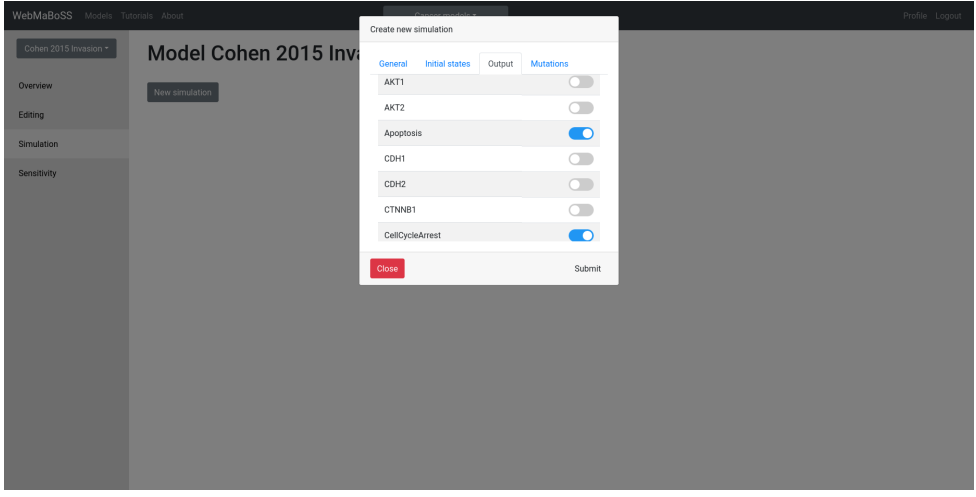
› Creating a new simulation : General settings



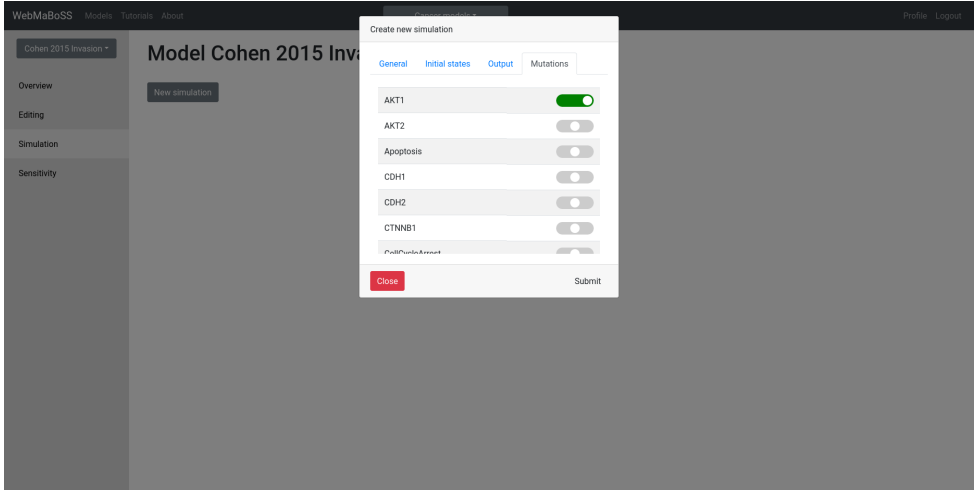
› Creating a new simulation : Initial states



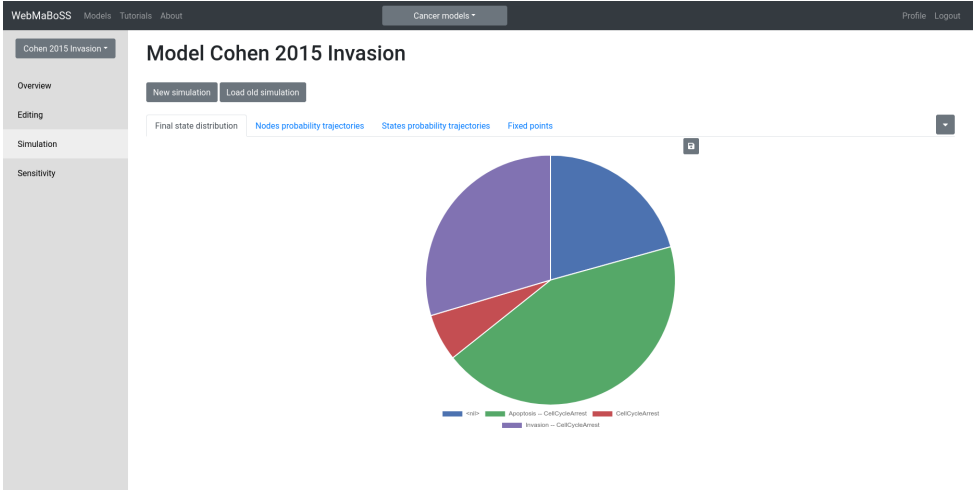
Creating a new simulation : Output nodes



› Creating a new simulation : Mutants

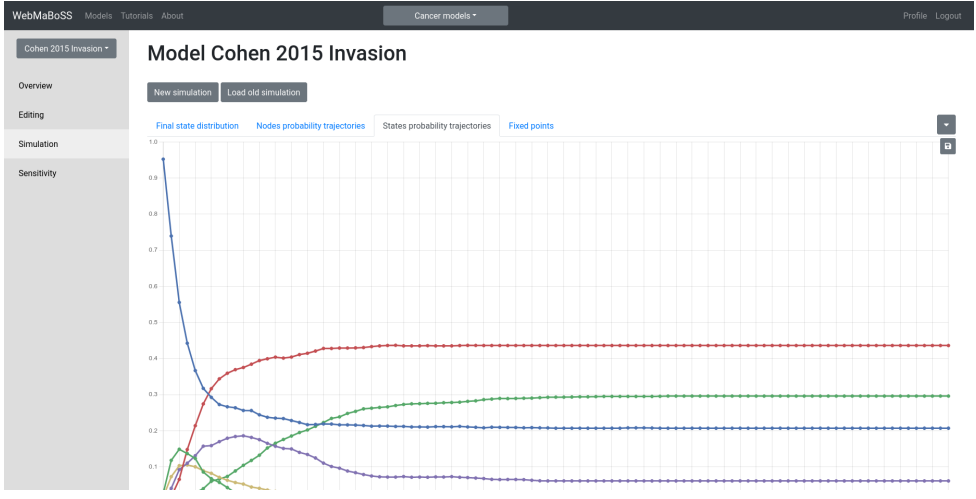


› Simulation results : Final states

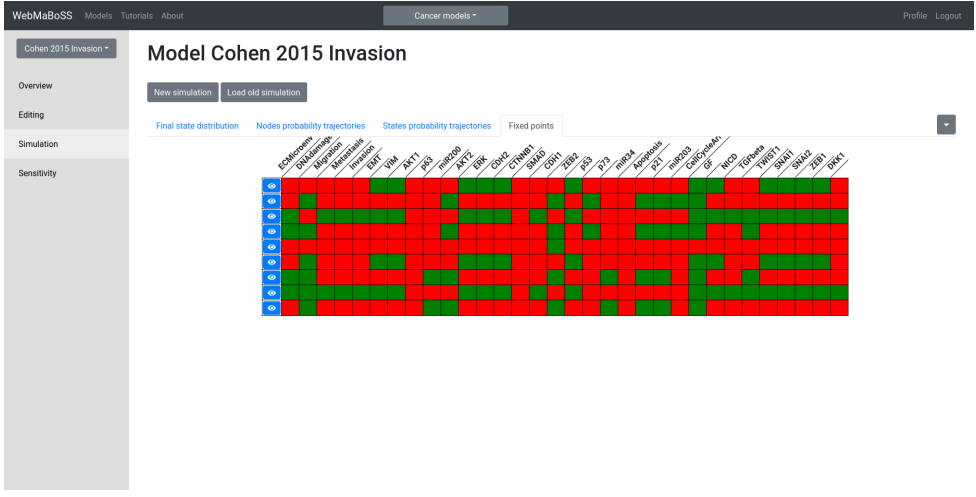


› Simulation results : Node trajectories

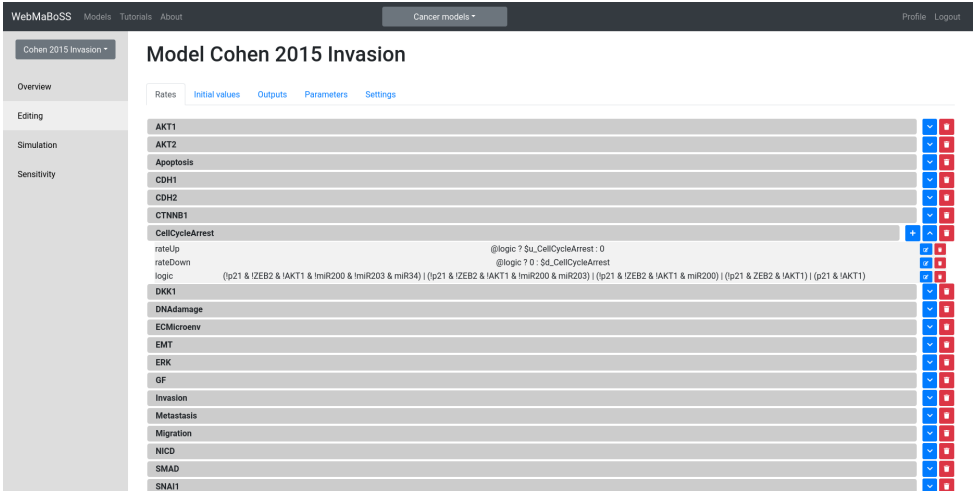
› Simulation results : State trajectories



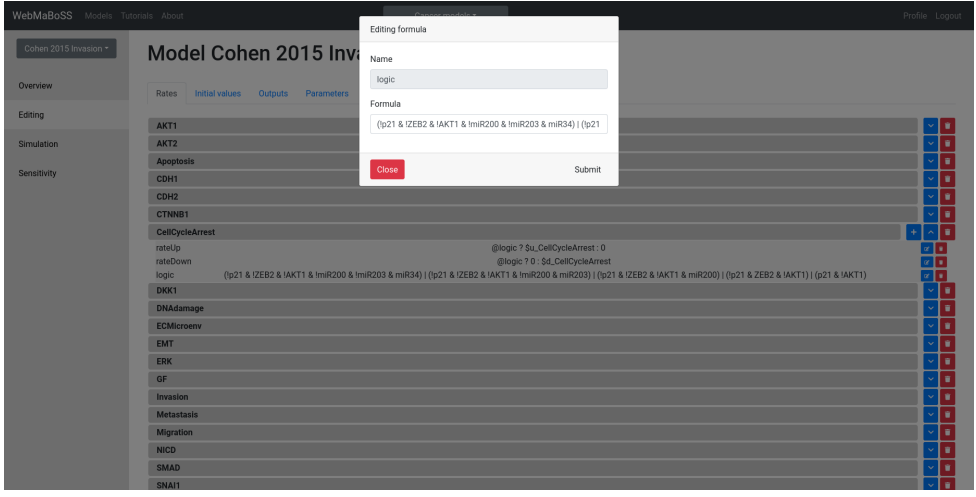
› Simulation results : Fixed points



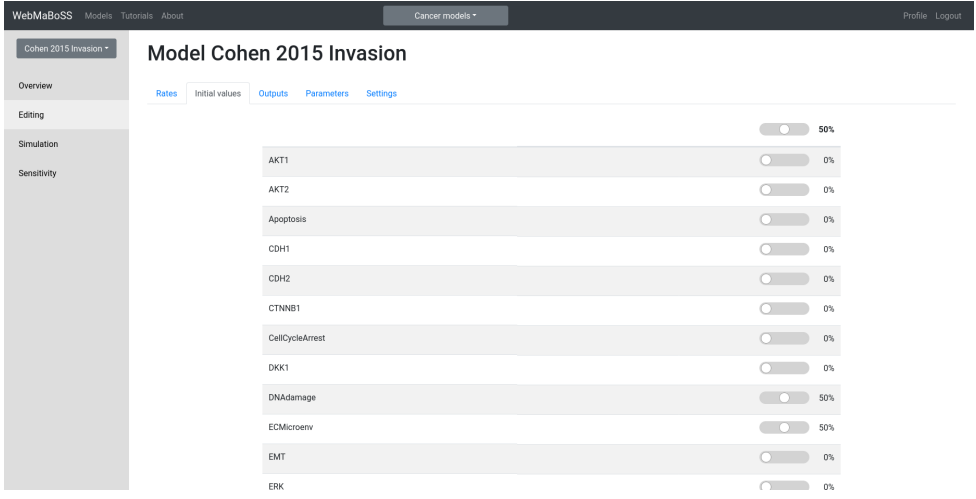
› Model editing : (in)activation rules



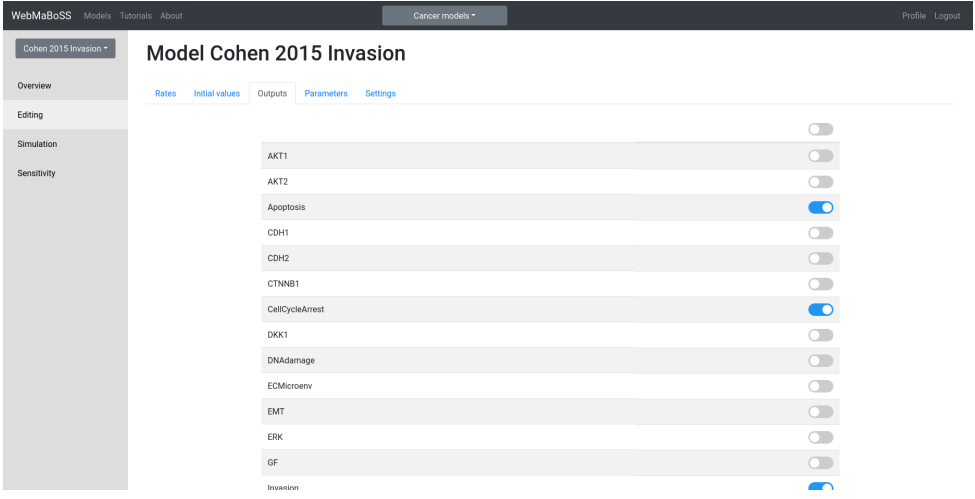
› Model editing : (in)activation rules



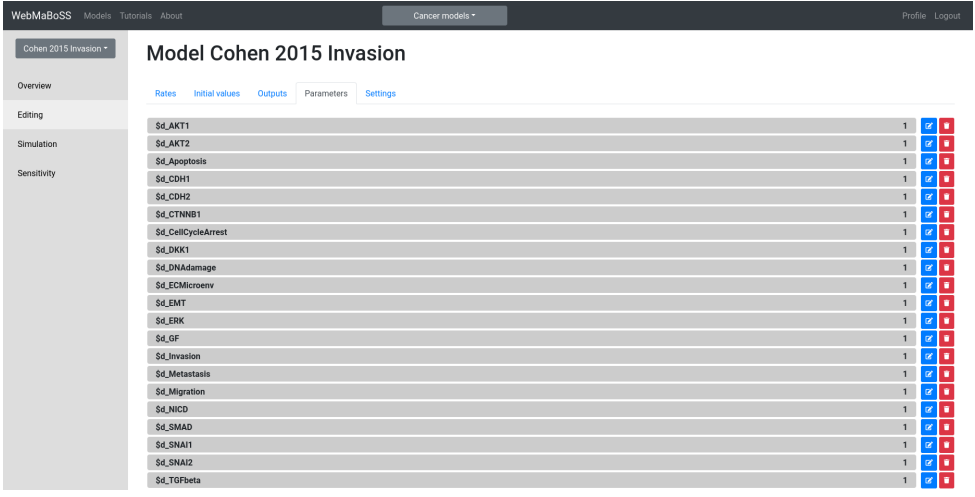
› Model editing : Initial states



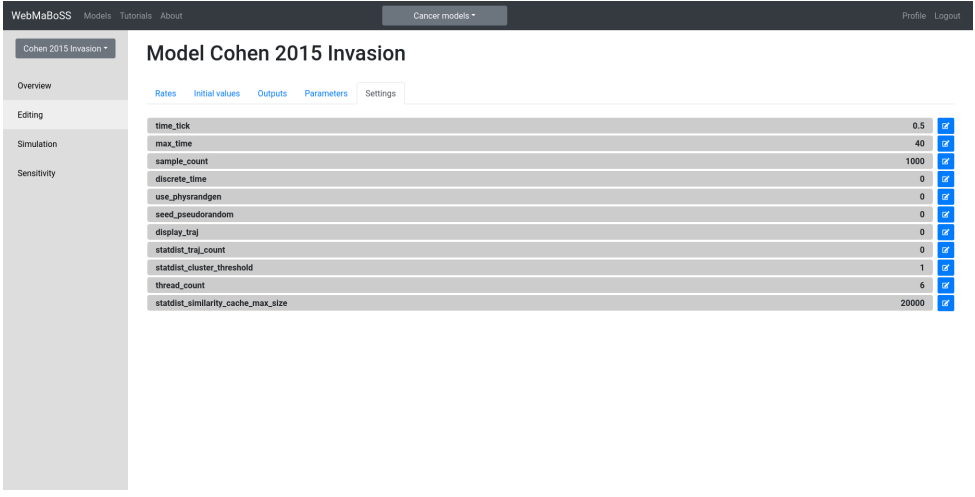
Model editing : Output nodes



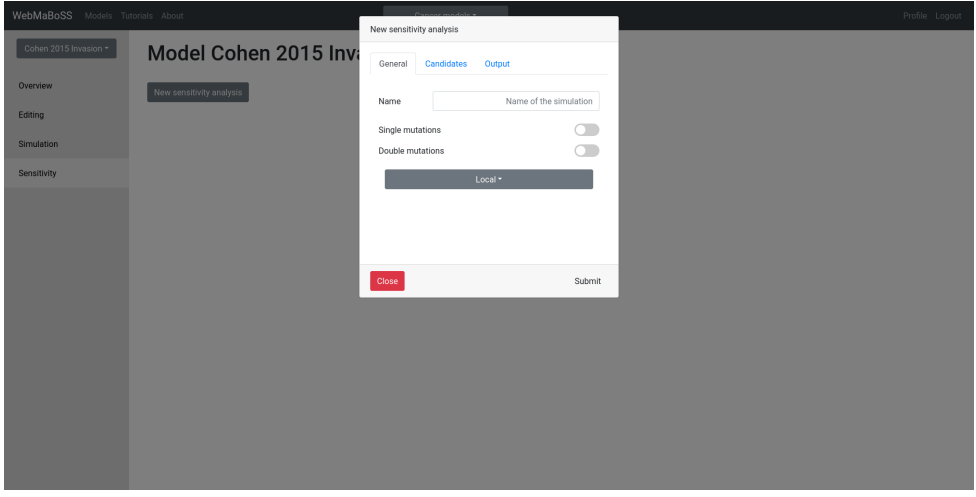
› Model editing : Parameters



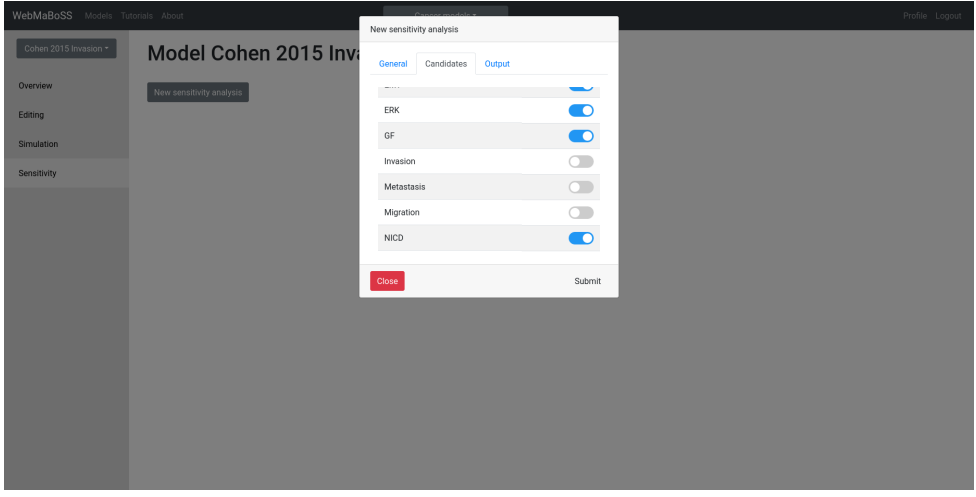
› Model editing : Settings



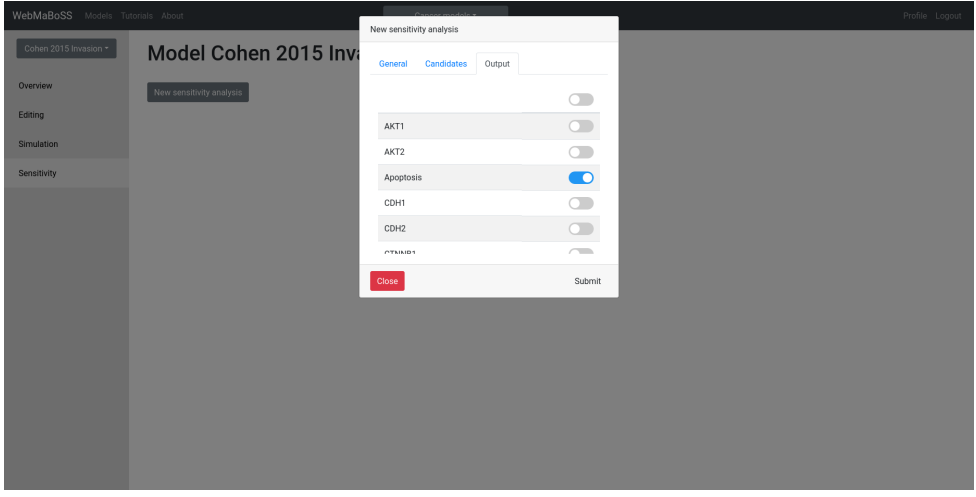
› Sensitivity analysis : General settings



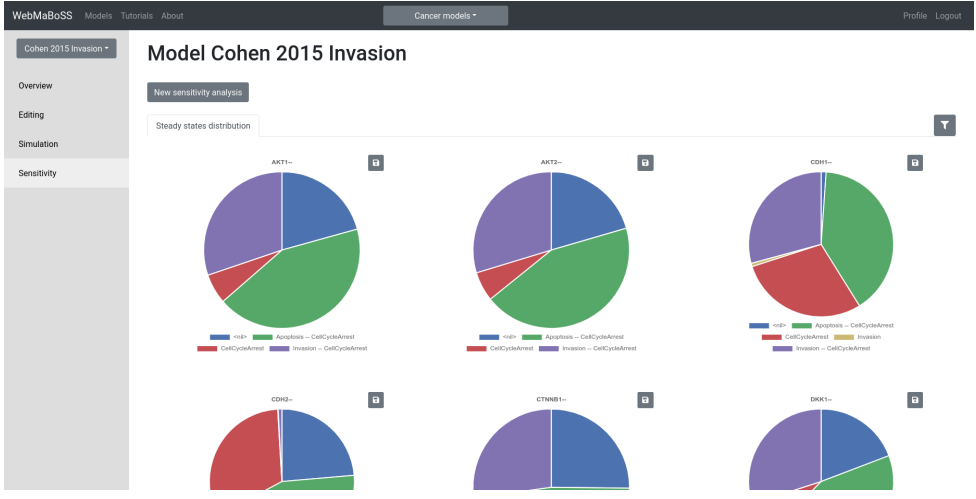
Sensitivity analysis : Mutant candidates



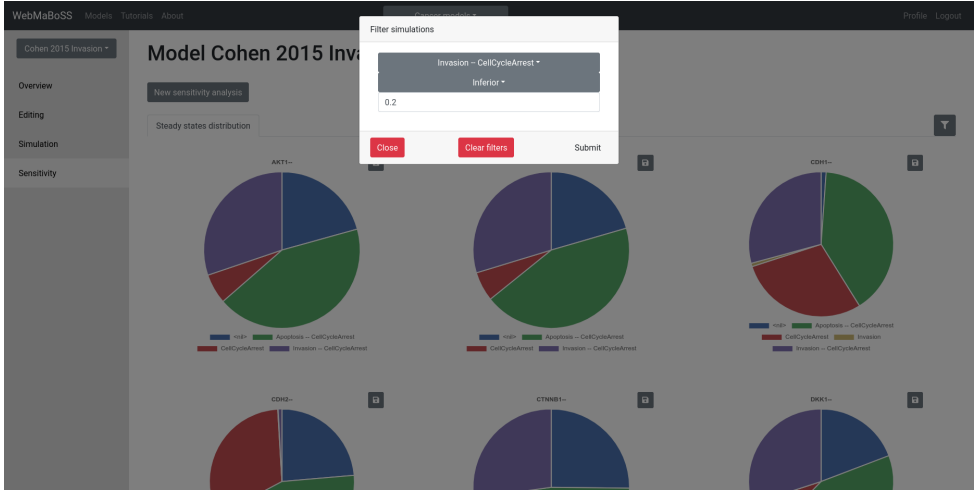
Sensitivity analysis : Output nodes



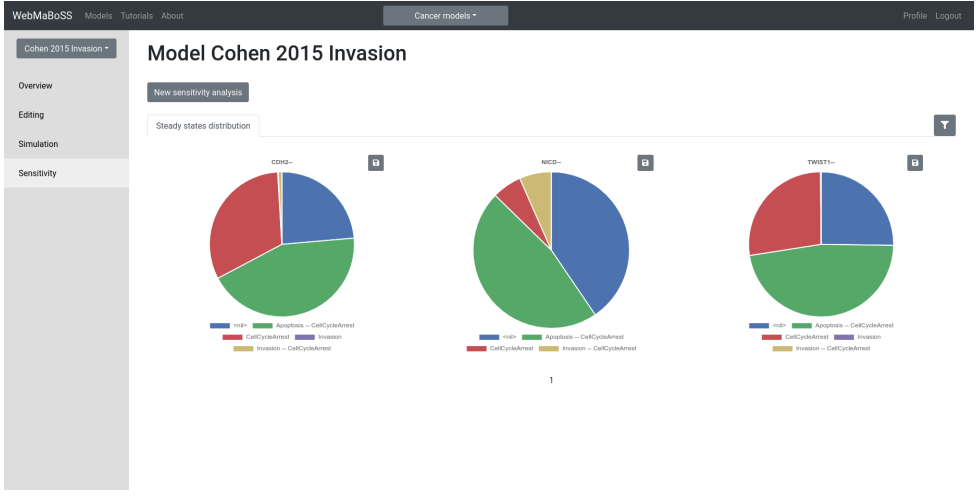
› Sensitivity analysis : Results



› Sensitivity analysis : Filtering results



› Sensitivity analysis : Filtered results



- Hands on
  - Create a new project
  - Load Cohen's model (bnd and cfg available in google drive)
  - Perform default simulation, report CellCycleArrest state final percentage
  - Perform simulation with ECMicroenv and DNADamage on, report Apoptosis node final percentage
  - Perform simulation with NICD++, p53– mutant, report number of fixed points

- Hands on
  - Perform sensitivity analysis on single mutants, testing only inhibitions
  - Filter mutants where state Invasion – CellCycleArrest is less than 20%
  - Report mutants found with such phenotypes